

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 9, 2002, 17:56:19 ; Search time 2638 Seconds
(without alignments)

6385.846 Million cell updates/sec

Title: US-09-635-501-2

Perfect score: 4291

Sequence: 1 MSSSSWLLSLVAVTAAGST.....ISKGNNPGFQNTDDVQVSF 805

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters: -DEV=xlh

-MODEL=frame+p2n.model -DEV=xlh

-Q/cgcn2_1/USFIO.spool/US09635501/runat_09102002_094529_18524/app_query.fasta_1.967

-DB=GenEmbl -OFMT=fastap -SUFFIX=rg -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0

-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45

-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL

-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000

-USFR=US09635501.ecgn.1.1714.0runat_09102002_094529_18524 -ICPU=3

-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120

-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7

-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*

1: gb.ba:*

2: gb.htg:*

3: gb.in:*

4: gb.om:*

5: gb.ov:*

6: gb.pat:*

7: gb.ph:*

8: gb.pl:*

9: gb.pr:*

10: gb.ro:*

11: gb.sts:*

12: gb.sy:*

13: gb.un:*

14: gb.vi:*

15: em.ba:*

16: em.fun:*

17: em.hum:*

18: em.in:*

19: em.mu:*

20: em.un:*

21: em.or:*

22: em.ov:*

23: em.pat:*

24: em.ph:*

25: em.pl:*

26: em.ro:*

27: em.sts:*

28: em.un:*

29: em.vi:*

30: em.htg.hum:*

31: em.htg.inv:*

32: em.htg.other:*

33: em.htgo.inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	4291	100.0	2415	6 ARI35178	ARI35178 Sequence
2	4291	100.0	2415	6 E43987	E43987 ACE-analogo
3	4291	100.0	2418	6 E39033	E39033 MPROT15 pol
4	4291	100.0	2599	6 E43988	E43988 ACE-analogo
5	4291	100.0	3325	9 AF291820	AF291820 Homo sapi
6	4291	100.0	3334	6 AX047758	AX047758 Sequence
7	4291	100.0	3396	6 ARI35177	ARI35177 Sequence
8	4291	100.0	3405	9 AF241254	AF241254 Homo sapi
9	4288	99.9	2599	9 AB046569	AB046569 Homo sapi
10	4281	99.8	3341	9 HSM800880	AL110224 Homo sapi
11	3740.5	87.2	2262	6 E39034	E39034 MPROT15 pol
12	3579	83.4	2638	6 AX047762	AX047762 Sequence
13	3562	83.0	2760	10 AB053181	AB053181 Mus muscu
14	3561	83.0	2638	6 AX047765	AX047765 Sequence
15	3509	81.8	2415	6 AX047760	AX047760 Sequence
16	2904	67.7	2415	6 AX047764	AX047764 Sequence
17	2167	50.5	1993	10 AB053182	AB053182 Mus muscu
18	1344	31.3	2473	9 HUMTACEA	M26657 Human testi
19	1344	31.3	2477	9 HSACE	X16295 Human mRNA
20	1344	31.3	2478	6 A31567	A31567 H.sapiens t
21	1344	31.3	2478	6 AR037213	AR037213 Sequence
22	1337	31.2	4020	6 ARI37383	ARI37383 Sequence
23	1337	31.2	4020	9 HUMAICEB	J04144 Human angio
24	1337	31.2	4024	6 A00914	A00914 H.sapiens g
25	1334	31.1	2418	10 MUSACEC	M55333 Mouse testi
26	1334	31.1	3813	10 MUSACEA	J04946 Mouse angio
27	1334	31.1	3939	6 AX147531	AX147531 Sequence
28	1334	31.1	4563	6 AX147503	AX147503 Sequence
29	1334	31.1	4694	10 MUSACEB	J04947 Mouse angio
30	1322	30.8	2551	9 HUNTACEC	M29981 Human aberr
31	1312	30.6	4050	5 CHKACEI	L40175 Gallus gall
32	1310	30.5	4014	10 AF201331	AF201331 Rattus no
33	1310	30.5	4014	10 AF201332	AF201332 Rattus no
34	1310	30.5	4014	10 RNU03708	U03708 Rattus norv
35	1310	30.5	4142	10 RNU03734	U03734 Rattus norv
36	1303	30.4	2490	9 HUMTACEB	M26658 Human testi
37	1283.5	29.9	4803	4 OCANCEB	X62551 O.cuniculus
38	1283	29.9	2409	4 RABACEA	J05041 Rabbit angli
39	1099.5	25.6	2211	3 AB026110	AB026110 Bombyx mo
40	1090	25.4	2001	3 DMU25344	U25344 Drosophila
41	1086	25.3	2002	3 AX061129	U061129 Drosophila
42	1061	24.7	1998	3 DMU34599	U34599 Drosophila
43	1058	24.7	2664	3 HMBH1PR	U43965 Haematobia
44	1057	24.6	4387	3 BMU62809	U62809 Boophilus m
45	1030	24.0	2452	3 DMACERMET	X96913 D.melanogas

ALIGNMENTS

RESULT 1	ARI35178	Sequence 3	from patent US 6194556.	2415 bp	DNA	linear	PAT 16-MAY-2001
LOCUS	ARI35178	Sequence					
DEFINITION	ARI35178						
ACCESSION	ARI35178						
VERSION	ARI35178.1						
KEYWORDS							
SOURCE	Unknown.						
ORGANISM	Unknown.						

Unclassified.	
REFERENCE	1 (bases 1 to 2415)
AUTHORS	Acton, S. Laurene and Robison, K. Earl.
TITLE	Angiotensin converting enzyme homolog and therapeutic and diagnostic uses therefor
JOURNAL	Patent: US 6194556-A 3 27-FEB-2001;
FEATURES	Location/Qualifiers
source	1..2415
BASE COUNT	743 a 483 c 555 g 634 t
ORIGIN	/organism="unknown"
Alignment Scores:	
Pred. No.:	0 Length: 2415
Score:	4291.00 Matches: 805
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	100.00% Indels: 0
DB:	6 Gaps: 0
US-09-635-501-2 (1-805) x AR135178 (1-2415)	
QY	1 MetSerSerSerSerTrpLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20
DB	1 ATGTCAAGCTCTTCCCTGGCTCTCTCAGCCCTGTGTGCTTAACCTGCTCAGTCCACC 60
QY	21 IleGluGluAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe 40
DB	61 ATTGAGCAACAGCCCAAGACATTTTGGACAAGTTTAACCAAGCAAGCCGAGAGACCTGCTC 120
QY	41 TyrGlnSerSerLeuAlaSerTrpAsnThrAsnThrAsnIleThrGluGluAsnValGln 60
DB	121 TATCAAAAGTTCACTGCTTCTTGGAAATTAACACCAATATATTACTGAAGAAATGTCCAA 180
QY	61 AsnMetAsnAlaGlyAspLysTrpSerAlaPheLeuLysLysLysLysLysLysLysLys 80
DB	181 AACATGAATAATGCTGGGCAACAATGGTCTGCCCTTTTAAAGGAACACTCCACACTTGC 240
QY	81 GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuAlaLeu 100
DB	241 CAATGTATCCACTACAGAATAATTCAGAAATCTCAGAGTCAAGCTTCAGCTCAGGCTCTT 300
QY	101 GlnGlnAsnGlySerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu 120
DB	301 CAGCAAAATGGCTTCAGTCTGTCTCAGAGACAGACAGCAACGGTTGAACACAAATCTA 360
QY	121 AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu 140
DB	361 AATACAATGAGCAACCATCTACAGTACTGGAAAAGTTTGTAAACCCAGATAAATCCACAAGAA 420
QY	141 CysLeuLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu 160
DB	421 TGCTTATTAATGAACCAAGTTTGAATGAATAATGGAACACAGTTTGAATACATCAATGAG 480
QY	161 ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr 180
DB	481 AGGCTCTGGGCTTGGGAAAGCTGGAGATCTGAGGTGGGCAAGCAAGCTTATATATATATAT 540
QY	181 GluGlnTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly 200
DB	541 GAACAGTATGTGCTTGTGAATAATGAGATGGCAAGCAAGCAATCATATTATGAGGACTATGG 600
QY	201 AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly 220
DB	601 GATTATTGGAGAGAGACTATCAAGTAAATGGGGTAGATGGCTATGACTACAGCGCGGCG 660
QY	221 GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu 240
DB	661 CAGTTGATTGAAGATGTGGACATACCTTTGAAGAGATTAACCAATATATATGACATCTT 720
QY	241 HisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly 260
DB	721 CATGCCATATGTAGGCAAGTTGATGAATGCTATCCTTCTATATCAGTCCCAATTTGGA 780
QY	261 CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer 280
DB	781 TGCCCTCCCTGCTCATTTGCTGTGTATATGTGGGTAGATTTTGGACAATCTGTACTCT 840
QY	281 LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln 300
DB	841 TTGACAGTTCCCTTTGGACAGAAACCAACATAGATGTTACTGATGCAATGCTGGACCAG 900
QY	301 AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu 320
DB	901 GCCCTGGATGCACAGAGAATAATTCAAGAGGCCGAGAAAGTTCTTTGATCTCTGTGGTCTT 960
QY	321 ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyValGln 340
DB	961 CCTATATGACTCAAGGATCTGGGAAATTCCTCTACCGACCCAGGAATGTTCCAG 1020
QY	341 LysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet 360
DB	1021 AAAGCAGTCTGCCATCCACAGCTTGGGACCTGGGAAAGGCGACTTCAGGATCCTTATG 1080
QY	361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln 380
DB	1081 TGCACAAAGGTGACAATGGAGACTTCTCTGACAGCTCATCATGAGATGGGCATATCCAG 1140
QY	381 TyrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe 400
DB	1141 TATGATATGTCATATGTCGACCAACCTTTTCTGCTAAGAAATGGAGCTTAATGAAGGATTC 1200
QY	401 HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer 420
DB	1201 CATGAAGCTGTGGGAAATCATGTCTTCTGACGCCACACCTTAAGCATTTAAATATCC 1260
QY	421 IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu 440
DB	1261 ATTGCTCTTCTGTCACCCGATTTTCAAGAGACAATGAACAGAAATAAATCTCTCGTCTC 1320
QY	441 LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg 460
DB	1321 AAACAAGCACTACAGATTTGTTGGGACTCTGCCATTTTACTTACATCTTAGAGAAGTGGAG 1380
QY	461 TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet 480
DB	1381 TGGATGGCTTTAAAGGGGAAATCCCAAGACCACTGGATGAAAGAGTGGTGGGAGATG 1440
QY	481 LysArgGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPro 500
DB	1441 AAGCGAGAGATAGTTGGGGTGGTGGAAACCTGTGCCCCATGATGAACACATCTGTGACCCC 1500
QY	501 AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu 520
DB	1501 GCATCTCTGTTCCATGTTTCTAATGATTACTCATTTCTCATATTACACAGGACCCCTT 1560
QY	521 TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis 540
DB	1561 TACCAATTTCCAGTTCGAAGAGCACTTTGTCAAGCAGCTTAAACATGAAGGCCCTCTGCAC 1620
QY	541 LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeu 560
DB	1621 AAATGTGACATCTCAAACTCTACAGAAGCTGGACAGAACTGTTCAATATGCTGAGGCTT 1680
QY	561 GlyLysSerGluProThrThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsn 580
DB	1681 GCAAAATCAGAACCCCTGGACCCCTAGCATTTGGAAATGTTGTAGGAGCAAGAAACATGAAT 1740
QY	581 ValArgProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLys 600
DB	1741 GTAAGGCCACTGTCAACTACTTTGAGCCCTTATTTTACCTGGCTGAAGACCAAGCAAG 1800
QY	601 AsnSerPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysVal 620
DB	1801 AATCTCTTTTGGGATGGATACCGACTGGGTCCATATGACAGCAAGCAAGCATCAAGTG 1860

621 ArgIleSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMet 640
Db 1861 AGGATAAGCCATAAATCAGCTCTGGAGATAAGCATATGATGAGACGACAAATGAATG 1920
Qy 641 TyrLeuPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsn 660
Db 1921 TACCTGTTCGATCATCTGTTCATATGCTATGAGGAGTACTTTTAAAGTAAAAAT 1980
Qy 661 GlnMetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSer 680
Db 1981 CAGATGATCTTTTGGGAGGAGATGTGGAGTGGCTAATTTGAACCAAGAAATCTCC 2040
Qy 681 PheAsnPheValThrAlaProLysAsnValSerAspIleLeuProArgThrGluVal 700
Db 2041 TTTAATTTCTTGTCACTGCACCTAAATAATGTGCTGATATCATCTCTAGACTGAAT 2100
Qy 701 GluLysAlaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsn 720
Db 2101 GAAAGGCCATCAGGATGTCCCGAGCGGTATCAATGATGCTTTCCGCTGGAATGACAAC 2160
Qy 721 SerLeuGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSer 740
Db 2161 AGCCTAGATTTCTGGGATACACCAACACTGGACCTCTAACCGCCCCCTGTTC 2220
Qy 741 IleTrpLeuIleValPheGlyValValMetGlyValIleValIleValIleLeu 760
Db 2221 ATATGGCTGATGTGTTTTGGAGTGTGATGGAGTGATGCTGGCATTTGTCATCC 2280
Qy 761 IlePheThrGlyIleArgAspArgLysLysLysAsnLysAlaArgSerGlyGluAsnPro 780
Db 2281 ATCTTCACTGGGATCAGAGATCGGAAGAGAAATAAAGCAAGAGTGGAGAAATCCT 2340
Qy 781 TyrAlaSerIleAspIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAsp 800
Db 2341 TATGCCCTCCATCGATATTAGCAAGGAGAAATAATCCAGGATTCCAAAACACTGATGAT 2400
Qy 801 ValGlnThrSerPhe 805
Db 2401 GTTCAGACCTCCTTT 2415

RESULT 2
E43987
LOCUS E43987 2415 bp DNA linear PAT 31-JAN-2002
DEFINITION ACE-analogous gene.
ACCESSION E43987
VERSION E43987.1 GI:18629190
KEYWORDS JP 2001046072-A/1.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2415)
AUTHORS Sugano,S. and Komatsu,T.
TITLE ACE-analogous gene
JOURNAL Patent: JP 2001046072-A 1 20-FEB-2001;
OTSUKA PHARMACEUT CO LTD
COMMENT OS Unknown
PN JP 2001046072-A/1
PD 20-FEB-2001
PR 06-AUG-1999 JP 1999223892
PI SUNIO SUGANO,TAKAMI KOMATSU
PC C12N15/09,A61K31/00,A61K31/7088,A61K38/00,A61K38/55,
A61K39/395, PC A61K39/395,
PC A61K39/395,A61K48/00,A61P9/12,C07K14/47,C07K16/08,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12Q1/68,G01N33/53,C12N15/00,A61K37/02, PC
A61K37/64,
PC C12N5/00
CC

Key Location/Qualifiers
FH key 1..2415
FT source /organism='Unknown'.
FT Location/Qualifiers

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/organism='unidentified'
/db_xref='taxon:32644'
BASE COUNT 743 a 484 c 554 g 634 t
ORIGIN
Alignment Scores:
Pred. No.: 0 Length: 2415
Score: 4291.00 Matches: 805
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0
US-09-635-501-2 (1-805) x E43987 (1-2415)
Qy 1 MetSerSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20
Db 1 ATGTCAAGCTCTCTCTGGCTCTCTCTCAGCCCTGTTGCTGTAACCTGCTCAGTCCACC 60
Qy 21 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe 40
Db 61 ATTGAGAAACAGCCCAAGACATTTTGGACAAGTTTAAACCAGACGACCGACCTGTTC 120
Qy 41 TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln 60
Db 121 TATCAAAGTTCATCTGCTTCTTGGAAATTAACACCAATATTACTGAAGAGAAATGTCAA 180
Qy 61 AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla 80
Db 181 AACATGAATTAATGCTGGGACAAATGGTCTGCTTTTAAAGAACACGTCACACTTCCC 240
Qy 81 GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuAlaLeu 100
Db 241 CAAATGTATTCACACTCAAGAAATTCAGAAATCTCAGATCTCAGCTCAAGCTTCAGCTG 300
Qy 101 GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu 120
Db 301 CAGCAAAATGGTCTTTCAGTGTCTCAGAGAACAGAGCAACGGTTGAACACAATCTA 360
Qy 121 AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu 140
Db 361 AATACAATGAGCACCATCTACAGTACTTGCAAAAGTTTGTACCCAGATAATCCACAAGAA 420
Qy 141 CysLeuLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu 160
Db 421 TGCCTATTACTTGAACACAGGTTTGAATGAAATTAATGGCAACAGTTTACACTACAATGAG 480
Qy 161 ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr 180
Db 481 AGGCTCTGGGCTTGGGAAAGCTGGAGATCTGAGGTGCGCAAGCAGCTGAGGCCATTATAT 540
Qy 181 GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly 200
Db 541 GAAGAGTATGTGCTTGAATAATGAGATGCAAGACGCAAAATCATTTATGAGGACTATGG 600
Qy 201 AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly 220
Db 601 GATTATTGGAGAGGAGACTATGAAGTAAATGGGTAGATGGCTATGACTAGACCGCGGC 660
Qy 221 GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu 240
Db 661 CAGTTGATTGAAGATGTGGACATACCTTTGAGAGAGATTAAACCATTTATATGACATCTT 720
Qy 241 HisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly 260
Db 721 CATGCTATGTGAGGGCAAAAGTTGATGAATGCCATCTCTCTATATCAGTCCAATGGA 780
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Db 781 TGCCTCCCTGCTCATTTGCTTGGGTGATATGTTGGGTGATTTTGGACAAATCTGTACTCT 840
Qy 281 LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln 300

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Db 841 TTGACAGTCCCTTTGGACAGAAACCAACATAGATTGTACTGATCAATGTGGACAG 900
QY 301 AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPheValSerValGlyLeu 320
Db 901 GCCTGGGATGCACAGAGAAATATCAAGGAGCGCGAGAAATCTTTGTATCTCTGTGGTCTT 960
QY 321 ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln 340
Db 961 CCTAATATGACTCAAGGATTTCTGGGAAATTTCCATGCTACAGGCCACCGAAGATGTTCAAG 1020
QY 341 LysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet 360
Db 1021 AAAGCAGTCTGCCATCCACAGCTTGGGACCTGGGGAAGCGGACATTCAGGATCCTTATG 1080
QY 361 CysThrLysValThrMetAspPheLeuThrAlaHisGluMetGlyHisIleGln 380
Db 1081 TGCACAAAGGTGACATGGAGGACTTCTGCACAGCTCATCATGAGATGGGGCATATCCAG 1140
QY 381 TyrAspMetAlaTyrAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe 400
Db 1141 TATGATATGGCATATGCTGCACACCTTTCTGCTAAGAAATGGAGCTAATGAAGGATTC 1200
QY 401 HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer 420
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QY 421 IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu 440
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QY 461 TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTyrTrpGluMet 480
Db 1381 TGGATGGTCTTTAAAGGGGAAATTTCCAAAGACCAGTGGATGAAAGAGTGGTGGAGATG 1440
QY 481 LysArgGluIleValGlyValGluProValProHisAspGluThrTyrCysAspPro 500
Db 1441 AAGCGAGAGATAGTGGGGTGGTGAACCTGTGCCCATGATGAACATATCTGTGACCCC 1500
QY 501 AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu 520
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Db 1561 TACCAATTCAGTTCAGAGACACTTTGTCAAGCAGCTTAACATGAAGGCCCTCTGCAC 1620
QY 541 LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeu 560
Db 1621 AATATGACATCTCAAACTCTACAGAGCTGGACAGAACTGTTCAATATATCTCAGGCTT 1680
QY 561 GlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsn 580
Db 1681 GGAAATTCAGAACCCCTGGACCTTAGCATTTGGAAAAATGTTGAGGACGAAAGAAATCAAT 1740
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Db 1741 GTAAGGCCACTGCTCAACTTCTTAGCCCTTATTTAGCCCTTATTTAGCTGGCTGAAGACCAACAG 1800
QY 601 AsnSerPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysVal 620
Db 1801 AATCTTTTGGGATGGAGTACCGACTGGAGTCCATATGACAGCAACCAAGCATCAAGTG 1860
QY 621 ArgIleSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMet 640
Db 1861 AGGATAAGCCCTAAATCAGCTCTTTGGAGATAAAGCATATGAATGAAGCAATCAAAATG 1920
QY 641 TyrLeuPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsn 660
|||||

Db 1921 TACTGTTCGATCATCTGTTCATATGCTATGAGCAGTACTTTTTTAAAGCTAAAAAT 1980
QY 661 GlnMetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSer 680
Db 1981 CAGATGATCTTTTGGGAGGAGGATGTGCGAGTGGCTAAATTTGAAACCAAGAAATCTCC 2040
QY 681 PheAsnPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal 700
Db 2041 TTTAAATTTCTTCTCACTGCACCTAAAAATGTCTGTGATATCATCTCTAGAACTGAAGTT 2100
QY 701 GluLysAlaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsn 720
Db 2101 GAAAGGCCATCAGGATGTCCTCCGAGCCGCTATCAATGATGCTTTCCGCTGATGACAAC 2160
QY 721 SerLeuGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSer 740
Db 2161 AGCCTAGATTTCTGGGATACAGCAACACTTGGACCTCTTAACCCAGCCCTGTTTCC 2220
QY 741 IleTrpLeuIleValPheGlyValValMetGlyValIleValValGlyIleValIleLeu 760
Db 2221 ATATGGCTGATTTGTTTGGAGTTGTATGGGAGTGTATGTTGGCATTTGTCATCTCG 2280
QY 761 IlePheThrGlyIleArgAspArgLysLysLysAsnLysAlaArgSerGlyGluAsnPro 780
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QY 781 TyrAlaSerIleAspIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAsp 800
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QY 801 ValGlnThrSerPhe 805
Db 2401 GTTCAGACCTCCCTTT 2415
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LOCUS MPROT15 polypeptide and MPROT15 polynucleotide.
DEFINITION E39033
ACCESSION E39033
VERSION E39033.1 GI:13017695
KEYWORDS JP 1999318472-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 2418)
AUTHORS Christopher,D.S.N.N.
TITLE MPROT15 polypeptide and MPROT15 polynucleotide
JOURNAL Patent: JP 1999318472-A 1 24-NOV-1999;
SMITHKLINE BEECHAM CORP PUBLIC LTD CO
COMMENT OS Homo sapiens (human)
PN JP 1999318472-A/1
PD 24-NOV-1999
PF 22-JAN-1999 JP 1999014949
PR 13-MAY-1998 GB 9810373;2,18-AUG-1998 GB 9818009;4 PI
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PC A61K39/395,A61K45/00,A61K48/00,C07K14/47,C12P21/02,C12Q1/68,
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BASE COUNT 744 a 484 c 555 g 635 t
ORIGIN

Alignment Scores:

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 Score: 4291.00 Matches: 805
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 Best Local Similarity: 100.00% Mismatches: 0
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 DB: 6 Gaps: 0

US-09-635-501-2 (1-805) x E39033 (1-2418)

QY	1	MetSerSerSerTrpLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr	20
Db	1	ATGTCAGGCTCTCCCTGGCTCTCTCAGCCTGTGTGTAACCTGCTGCATCCACC	60
QY	21	IleGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe	40
Db	61	ATTGAGCAACAGCCCAAGACATTTTGGACAAGTTTAAACCAGGAAGCGAGACCTGTC	120
QY	41	TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln	60
Db	121	TATCAAAAGTTCACTGCTCTTGGAAATATAACACCAATATTAAGAGAAATGTCCTCA	180
QY	61	AsnMetAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla	80
Db	181	AACATGAATTAATGCTGGGACAAATGCTGCTGCTTTTAAAGGAACAGCTCCACACTGCC	240
QY	81	GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuAlaLeu	100
Db	241	CAATGCTATCCACTACAAGAAATTCAGAAATCTCAGAGTCAAGCTTCAGCTCGAGGCTCTT	300
QY	101	GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu	120
Db	301	CAGCAAAATGGGTCTTCAGTGCTCTCAGAGACAGACAGCAACGGTTGACACAAATCTA	360
QY	121	AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu	140
Db	361	AATCAATGAGCACCATCTACAGTACTGGAAGAGTTTGTAAACCAGATAATCCACAAGAA	420
QY	141	CysLeuLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu	160
Db	421	TGCTTATTAATGACACAGGTTTGAATGAATTAATGGAACAGTTTATGACTACATGAG	480
QY	161	ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr	180
Db	481	AGGCTCTGGGCTGGGAAGCTGAGATCTGAGGTGGGCGGCAAGCAGCTGAGGCCATTAT	540
QY	181	GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly	200
Db	541	GAAGAGTATGTGCTTGAATAATGAGATGGCAGAGCAAAATCATTAAGAGACTATGGG	600
QY	201	AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly	220
Db	601	GATTAATGGAGAGAGAGATATGAAGTAATGGGGTAGATGGCTATGACTACAGCCGGGC	660
QY	221	GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu	240
Db	661	CAGTGTGATGAAGATGGGAACATACCTTTGAAGAGATTAACACCATTAATGAACATCTT	720
QY	241	HisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly	260
Db	721	CATGCCCTATGTAGGGCAAGTTGATGAATGCTATCCTATCTATATCAGTCCCAATGGA	780
QY	261	CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer	280
Db	781	TGCCCTCCCTGCTCATTTGCTGTGATATGCTGGGTAGATTTTGGACAAATCTGTACTCT	840
QY	281	LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln	300
Db	841	TTGACAGTCCCTTTGGACAGAAACCAACATAGATGTTACTGATGCAATGGTGGACAG	900
QY	301	AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu	320
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Db	901	GCCTGGGATGCACAGAGAAATATCAAGAGGGCGGAGAGTCTCTTCTATCTGTTGGTCTT	960
QY	321	ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln	340
Db	961	CCTAATATGACTCAAGGATTCGGGAAATTCATCTCTAACGGACCCAGGAAATGTTTCAG	1020
QY	341	LysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet	360
Db	1021	AAAGCAGTCTGCCATCCACAGCTTGGACCTGGGAAAGGGGACTTCAGGATCCTTATG	1080
QY	361	CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln	380
Db	1081	TGCRAAAGGTGCAATGGAGCCTTCTGCACAGCTCATCATGAGATGGGCAATATCCAG	1140
QY	381	TyrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe	400
Db	1141	TATGATATGGCATATGCTGCACAACTTTTCTGCTAAGAAATGGAGCTTAATGAAGATTC	1200
QY	401	HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer	420
Db	1201	CATGAAGCTGTGGGAAATCATGTCACTTCTGCAGCCACACCTAAGCATTTAAATATCC	1260
QY	421	IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu	440
Db	1261	ATTGCTCTCTGTCACCCGATTTTCAAGAGACAAATGAACAGAAATAAATTCCTGCTC	1320
QY	441	LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg	460
Db	1321	AAACAAGCCTCAGCATGTGTGGGACTCTGCCATTTTACTTACATGTAGAGAAATGGAGG	1380
QY	461	TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet	480
Db	1381	TGGATGGCTTTTAAAGGGGAAATTCACAAAGACCACTGGATGAAGAAATGGTGGAGATG	1440
QY	481	LysArgGluIleValGlyValGluProValProHisAspGluThrTyrCysAspPro	500
Db	1441	AAGCGAGAGATAGTGGGGTGGAACTGTGCCCATGATGAACACATACCTGACCCC	1500
QY	501	AlaSerLeuPheHisValSerAspTyrSerPheIleArgTyrTyrThrArgThrLeu	520
Db	1501	GCATCTCTGTTCCATGTTTCTAATGATTACTCATTCATTCGATATTACACAGGACCCTT	1560
QY	521	TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis	540
Db	1561	TACCAATTTCCAGTTTCAAGAGCAGCTTTGCAAGCAGCTAAACATGAAGCCCTCTGCAC	1620
QY	541	LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeu	560
Db	1621	AAATGTGACATCTCAAACTCTACAGAGCTGGACAGAACTGTTCAATATGCTGAGGCTT	1680
QY	561	GlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsn	580
Db	1681	GGAAATCAGAACCCCTGACCTAGCATTTGGAATGTTGTAGGAGCAAGAACATGAAT	1740
QY	581	ValArgProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLys	600
Db	1741	GTAAAGCCCACTGCTCAACTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAAGAACAG	1800
QY	601	AsnSerPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysVal	620
Db	1801	AAATCTTTTGTGGATGGAGTACCGACTGAGTCCCATATGCAGACCAAGACATCAAGATG	1860
QY	621	ArgIleSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMet	640
Db	1861	AGGATAAGCCCTAAATCAGCTCTTTGGAGATAAAGCATATGAATGAAGCAACATGAATG	1920
QY	641	TyrLeuPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsn	660
Db	1921	TACCTGTTCCGATCATCTGTTGCATATGCTATGAGGCAGTACTTTTTTAAAGTAAAAAT	1980
QY	661	GlnMetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSer	680
Db	1981	CAGATGATCTTTTGGGGAGGAGGATGTGCGAGTGGCTAAATTTGAACCAAGAAATCTCC	2040

Qy	681	PheAsnPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal	700
Db	2041	TTTTAATTTCTTCTCACTGCACCTAAATAATGTCTGATATCATCTCTAGAACTGAAAGTT	2100
Qy	701	GluLysAlaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsn	720
Db	2101	GAAGAAGCCATCAGAGATGCCCGGAGCCGTATCAATGATGTCTTCGGTCTGTAATGACAAC	2160
Qy	721	SerLeuGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSer	740
Db	2161	AGCCTAGAGTTCTGGGATACAGCAACACACTGGACCTCTTAACCGAGCCCTGTCTTCC	2220
Qy	741	IleTrpLeuIleValPheGlyValValMetGlyValIleValValGlyIleValIleLeu	760
Db	2221	ATATGGCTGATGTTTTTGGAGTGTGATGGGAGTGATGTGGTGTGCATGTCTCTCTG	2280
Qy	761	IlePheThrGlyIleArgAspArgLysLysLysAsnLysAlaArgSerGlyGluAsnPro	780
Db	2281	ATCTTCACTGGGATCAGAGTCGAAGAAGAAAAATAAAGCAAGAAGTGGAGAAAAATCCT	2340
Qy	781	TyrAlaSerIleAspIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAsp	800
Db	2341	TATGCTTCCATCGATATTAGCAAGAGAGAAAAATAATCCAGGATTCCTCAAAACACTGATGAT	2400
Qy	801	ValGlnThrSerPhe	805
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DEFINITION			
ACE-analogous gene.			
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VERSION			
E43988.1 GI:18629191			
KEYWORDS			
JP 2001046072-A/2.			
SOURCE			
unidentified.			
ORGANISM			
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REFERENCE			
1 (bases 1 to 2599)			
Sugano,S. and Komatsu,T.			
AUTHORS			
Sugano,S. and Komatsu,T.			
TITLE			
ACE-analogous gene			
JOURNAL			
Patent: JP 2001046072-A 2 20-FEB-2001;			
OTSUKA PHARMACEUT CO LTD			
COMMENT			
OS Unknown			
PN JP 2001046072-A/2			
PD 20-FEB-2001			
PF 06-AUG-1999 JP 1999223892			
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PI SUMIO SUGANO,TAKAMI KOMATSU			
PC C12N15/09,A61K31/00,A61K31/7088,A61K38/00,A61K38/55,			
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PC C12N5/00			
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Score:			
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Matches:			
100.00%			
Conservative:			
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Best Local Similarity:			
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Query Match:			
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Indels:			
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Conservative:			
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Mismatches:			
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US-09-635-501-2 (1-805) x E43988 (1-2599)			
Qy	1	MetSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr	20
Db	55	ATGCAAGCTCTCTCGCTCCCTTCAGCCTGTGTGCTTAACCTGCTGCTCAGTCCACC	114
Qy	21	IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe	40
Db	115	ATTGAGGAACAGGCCAAGACATTTTGGACAAGTTTAAACCAGAACGCCGAGACCTGTTC	174
Qy	41	TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln	60
Db	175	TATCAAGTTCACCTGCTCTTGGAAATTAACACCAATATTACTGAAGAGAAATGCCAA	234
Qy	61	AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla	80
Db	235	AACATGAATATGCTGGGGACAAATGCTGCTCTTTTAAAGGAACAGTCCACACTTCCC	294
Qy	81	GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeu	100
Db	295	CAATGTATCCACATACCAAGAAATTCAGATCTCACAGTTCAGCTTCAGCTGCGGCTCTT	354
Qy	101	GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu	120
Db	355	CAGCAAAATGGGTCTTCAGTCTCTCAGAGACAGACAGCAAAACGGTTGAACACAATCTA	414
Qy	121	AsnThrMetSerThrIleTyrSerThrGlyLysValLysAsnProAspAsnProGlnGlu	140
Db	415	AATCAATGAGCACCATCTACAGTACTGGAAAAGTTTGAACCCAGATAATCCACAGAA	474
Qy	141	CysLeuLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGln	160
Db	475	TGCTTATTACTTGAACCCAGCTTTGAATGAAATAATGCAACAGTTTACACTACAAATGAG	534
Qy	161	ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr	180
Db	535	AGGCTCTGGGCTTGGGAAAGCTGAGATCTGAGGTGGGACAGCAGCTGAGGCCATATAT	594
Qy	181	GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly	200
Db	595	GAAGAGTATGTGGTCTTGAATAATGAGATGGCAAGAGCAAAATCAATTATGAGGACTATGG	654
Qy	201	AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly	220
Db	655	GATTATTGGAGAGGAGACTATGAAGTAAATGGGTAGATGGCTATGACTACAGCCGCGC	714
Qy	221	GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu	240
Db	715	CAGTTGATTGAAGATGTGGAACATACCTTTTGAAGAGATTAAACCATTTATATCAACATCTT	774
Qy	241	HisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly	260
Db	775	CATGCCATGTGAGGGCAAAAGTTGATGAATGCTATATCTCTTATATATCATGTCCTTGA	834
Qy	261	CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer	280
Db	835	TGCCTCCCTGCTCATTTGCTTGGTGATATGTGGGTAGATTTTGGACAAATCTGTACTCT	894
Qy	281	LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln	300
Db	895	TTGACAGTTCCTTTTGGACAGAAACCAACATAGATGTTACTGATGATGCTGATGGACAG	954
Qy	301	AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu	320
Db	955	GCCTGGGATGCACAGAGAAATATTCAGAGGAGCCGCGAGAAAGTTCTTGTATCTGTGCTCTT	1014
Qy	321	ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln	340
Db	1015	CCTAATATGACTCAAGGATTTCTGGGAAAATTCATGCTAACGAGACCCAGGAAATGTTCA	1074
Qy	341	LysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet	360

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QY 361 CysThrLysValThrMetAspPheLeuThrAlaHisHisGluMetGlyHisIleGln 380
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QY 401 HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer 420
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QY 421 IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu 440
Db 1315 ATTGGTCTTCTGTCACCCGATTTCAAGAAGACAAATGAACAGAAATAAACTTCTGCTC 1374
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Db 1375 AAACAAGCACTACGATGTTGGGACTCTGCCATTTACTTACATGTTAGAGAACTGGAGG 1434
QY 461 TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet 480
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QY 581 ValArgProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLys 600
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Db 1855 AAATCTTTTGTGGATGGAGTACCGACTGAGTCCATATGCGACCAAGCAATCAAGTG 1914
QY 621 ArgIleSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMet 640
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Db 2035 CAGATGATCTTTTGGGAGGAGGATGTCGAGTGGCTTAATTTGAAACCAAGCAATCTCC 2094
QY 681 PheAsnPheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal 700
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DEFINITION Homo sapiens ACE-related carboxypeptidase ACE2 mRNA, complete cds.
ACCESSION AF291820
VERSION AF291820.1 GI:9802432
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3325)
AUTHORS Donoghue,M., Heien,F., Baronas,E., Godbout,K., Gosselin,M.,
Stagiliano,N., Donovan,M., Woolf,B., Robison,K., Jeyaseelan,R.,
Breitbart,R.E. and Acton,S.
A novel angiotensin-converting enzyme-related carboxypeptidase
(ACE2) converts angiotensin I to angiotensin 1-9
Circ. Res. 87 (5), E1-E9 (2000)
JOURNAL PUBMED 20429895
MEDLINE 10969042
REFERENCE 2 (bases 1 to 3325)
AUTHORS Donoghue,M., Woolf,B., Robison,K. and Acton,S.
Direct Submission
TITLE Submitted (01-AUG-2000) Cardiovascular Biology, Millennium
Pharmaceuticals, Inc, 75 Sidney Street, Cambridge, MA 02139, USA
JOURNAL
FEATURES
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BASE COUNT 1022 a 637 c 747 g 919 t

ORIGIN

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US-09-635-501-2 (1-805) x AF291820 (1-3325)

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DEFINITION Sequence 1 from Patent WO0070032.
ACCESSION AX047758
VERSION AX047758.1 GI:11876765
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3334)
REFERENCE Fiddington,C.S., Petrie,C.R., Shoemaker,K.E. and Bishop,P.D.
TITLE zace2: a human metalloenzyme
JOURNAL Patent: WO 0070032-A 1 23-NOV-2000;
ZymoGenetics, Inc. (US)
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 VERSION AR135177.1 GI:14124082
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 3396)
 AUTHORS Acton,S.Laurene and Robison,K.Earl.
 TITLE Angiotensin converting enzyme homolog and therapeutic and
 diagnostic uses therefor
 JOURNAL Patent: US 6194556-A 1 27-FEB-2001;
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 library kaia clone:kaia4505.
 ORGANISM Homo sapiens
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS Suzuki,Y., Watanabe,M. and Sugano,S.
 TITLE Cloning, expression analysis and chromosomal localization of a novel ACE like enzyme
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 2599)
 AUTHORS Komatsu,T., Suzuki,Y. and Sugano,S.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUL-2000) Takami Komatsu, the Institute of Medical Science, Virology; 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:komatsu@ims.u-tokyo.ac.jp, tel:81-3-5449-5283(ex.75283), Fax:81-3-5449-5416)
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gene

CDS

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QY	141	CysLeuLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu	160		
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VERSION AL110224.1 GI:5817159
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SOURCE human.
ORGANISM
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 3341)
Wambutt,R., Heubner,D., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
Direct Submission
Submitted (15-AUG-1999) MIPS, Am Klopferspitz 18a, D-82152
Martinsried, GERMANY
COMMENT
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKFp434A014) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://www.mips.biochem.mpg.de/proj/cDNA/.
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AUTHORS Christopher, D.S.N.N.
TITLE MPR0T15 polypeptide and MPR0T15 polynucleotide
JOURNAL Patent: JP 1999318472-A 2 24-NOV-1999;
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PN JP 1999318472-A/2
PD 24-NOV-1999
PF 22-JAN-1999 JP 1999014949
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CHRISTOPHER D SAZAN, NICOLA BAGESU


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 ACCESSION AB053181
 VERSION AB053181.1 GI:13517092
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 REFERENCE 1 (sites)
 AUTHORS Komatsu, T., Sugano, S., Imai, J., Suzuki, Y., Hanaoka, K., Ymada, Y., Hida, M., Tanigami, A. and Muroi, S.
 TITLE Molecular cloning, mRNA expression, and chromosomal localization of mouse Angiotensin-converting Enzyme-Related Carboxypeptidase
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 2760)
 AUTHORS Komatsu, T., Sugano, S. and Suzuki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (04-JAN-2001) Takami Komatsu, The Institute of medical science, University of Tokyo, Laboratory of Genome Structure Analysis; 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan [E-mail:komatsu@ims.u-tokyo.ac.jp, Tel:81-3-5449-5283(ex.75283), Fax:81-3-5449-5416]
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ACCESSION AX047765
VERSION AX047765.1 GI:11876771
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ZymoGenetics, Inc. (US)
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 AX047760 2415 bp DNA linear PAT 15-DEC-2000
 LOCUS Sequence 3 from Patent WO0070032.
 DEFINITION AX047760
 ACCESSION AX047760
 VERSION AX047760.1 GI:11876767
 KEYWORDS synthetic construct.
 SOURCE synthetic construct.
 ORGANISM artificial sequence.
 REFERENCE 1 (bases 1 to 2415)
 AUTHORS Piddington,C.S., Petrie,C.R., Shoemaker,K.E. and Bishop,P.D.
 TITLE Zace2: a human metalloenzyme
 JOURNAL Patent: WO 0070032-A 3 23-NOV-2000;
 FEATURES ZymoGenetics, Inc. (US)
 LOCATION/Qualifiers
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 misc_feature
 1. .2415
 /note="n = A,T,C or G"

BASE COUNT 494 a 218 c 398 g 335 t 970 others
ORIGIN

Alignment Scores:

Pred. No.: 4, 01e-298 Length: 2415
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Percent Similarity: 80.00% Conservative: 0
Best Local Similarity: 80.00% Mismatches: 161
Query Match: 81.78% Indels: 0
DB: 6 Gaps: 0

US-09-635-501-2 (1-805) x AX047760 (1-2415)

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QY 41 TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln 60
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QY 61 AsnMetAsnAsnAlaGluAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla 80
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